

**Amendments to the Specification:**

Please replace the last full paragraph of page 10 with the following rewritten paragraph:

FIG. 4. M11L contains a COOH terminal mitochondrial targeting signal. COS-7 or HeLa cells expressing GFP-mt, a construct consisting of GFP tagged with the COOH terminal 25 amino acids of M11L (mt) containing the putative transmembrane domain (underlined), were visualized by confocal microscopy. The distribution of the GFP-mt (a and d) and Mitotracker red (b and e) was found to be coincident (c and f). Hence, the COOH terminal 25 amino acids of M11L are sufficient for mitochondrial targeting. Bars, 10 nm. The amino acid sequence is represented in the sequence listing as SEQ ID NO: 1.

Please replace the paragraph bridging pages 10-11 with the following rewritten paragraph:

FIG. 5. The M11L mitochondrial targeting signal belongs to a consensus found in other proteins. Proposed COOH terminal consensus for targeting Bcl-2 family members to the mitochondrial outer membrane. The COOH terminal sequences shown include those of the antiapoptotic Bcl-2 family members Bcl-2, BclX<sub>L</sub>, Boo/Diva, and CED-9, the viral antiapoptotic proteins M11L, BHRF1, and KSbcl-2, as well as the proapoptotic proteins Nip3 and Nix. The amino acid sequences (from top to bottom) are represented in the sequence listing as SEQ ID NOs: 8-16.

Please replace the 3<sup>rd</sup> full paragraph on page 12 with the following rewritten paragraph:

FIG. 10. MS spectra for a peptide analyzed by nanospray mass spectrometer in MS/MS mode. The amino acids are read from right to left and are determined from the mass difference between the ions shown. The amino acid sequence is represented in the sequence listing as SEQ ID NO: 1.

Please replace the 4<sup>th</sup> full paragraph on page 12 with the following rewritten paragraph:

FIG. 11. Amino acid sequence of BAK. The peptide shown on in FIG. 10 was VVALLGFGYR (SEQ ID NO: 1 ~~SEQ ID No. 4~~) and it was one of three peptides (shown here in bold) identified by nanospray mass spectrometry from the protein BAK. These three peptides are sufficient to confirm that BAK was the protein isolated from one of the bands analyzed. Other bands excised from the gel were analyzed by mass spectrometry in a similar fashion. The amino acid sequence is represented in the sequence listing as SEQ ID NO: 17.